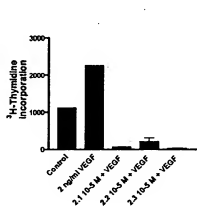
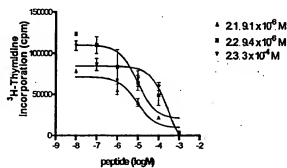


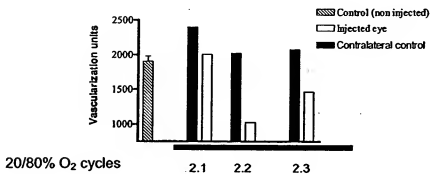
FIG. 1



A



B



C

FIG. 2

HQSKVLLAVALWLVCVETRAASVGLPSVSLDLPLRLSIQKDILTIRANTLTQITCRQRDL 60  
 ↑  
 Ig-like 1  
 WLVFNPNQSGSEQREVTECSDLGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVD 120  
 YRSPFFIASVSDQHGVVYITENKNKNTVVIPCLGSSISNLNVSLCARYPEKRFVPDGNRISWD 180  
 ↑  
 Ig-like 2  
 SKKGFTIPSYMHSIAGMVPCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 240  
 KLVLNCTARTELVNIGIDFNWEYPPSSKHQHKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300  
 ↑  
 Ig-like 3  
 DQGLYTCAASSGLMTKKKNSTFVRVHEKPFVAFPGSGMESLVEATVGERVRIPAKYLGYPPP 360  
 ↑  
 Ig-like 4  
EIKWYKNGIPLSENHTIKAGHVLTIMEVSRDGTGNYTVILTNPISEKQSHVSVLVVYVP 420  
PQIGEKSLISFPVDSYQYGTITLTCTCTVYAIPPPHHHWIWLQEBCANEPSQAVSVTNFY 480  
 ↑  
 Ig-like 5  
PCEHWRSVEDPQGGNKIEVKNQFALIEGKNKTVSTLVIQAA NVSALYKCEAVNKVGRGE 540  
RVISFHVTRGPBITLQPDMPTEQESVSLWCTADRSTFENLTWYKLGQPQLPIHVGE LPT 600  
 ↑  
 Ig-like 6  
FVCKNLDTLWKLNATMFSNSTMDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVFVRQLT 660  
 ↓  
 Ig-like 7  
 VLERVAPTITGNLENOTTSIGESIEVSC TASNPPPOIMNFKDNKTLVRDSGIVLKDGNR 720

NLTIIRVRKEDGLYTCQACSVLGC AKVKAFFIIEGAQEKTNLEI ILVGTAVIAMPFNL 780  
 LLVITILRTVKRANGGELKTGYLSIVMDPDELPLDERCERLPYDASKWEFFPRDLKLGKPL 840  
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLREGATHSEHRALMSELKILIHIGHLNVVN 900  
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQCKDYVGAIPVDLK 960  
 RRLDSITSSQSSASSGFVVEKSLSDVEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020  
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR 1080  
 VITIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTM 1140  
 DCWHEGPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200  
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTS 1260  
 GMVLASEELKTLEDRTKLSPSPFGMVPSKSRRESVASRGSNQTSQYSGYHSDDTDTTVYS 1320  
 SEEAELKLIIEIGVQTGSTAQILQPDSGTTLSSPPV

FIG. 3 continued

MKVLLRLICFIALLISSLEADKCKEREKKIILVSSANEIDVRPCPLNPNKHKGTTITWKD 60  
 ↑  
 Ig-like domain 1 →  
 DSKTPVSTEQASRIHQHKEKLWFVPKVEDSGHYTCVVRNSSYCLRIKISAKFVENEPNL 120  
 CTNAQAIKQKLPVAGDGGGLVCPYMEFFKNENNELPKLQWYKDCPLLLDNIHPSGVKDR 180  
 ↑  
 Ig-like 2 →  
LIVMNVAEKHRCNYTCHASYTYLGGQYPITRVIEFITLEENKPTRPVIVSPANETMEVDL 240  
 ↑  
 Ig-like 3 →  
 GSQIQLICNVGTGQLSDIAYWKNWGSVIDEDDPVLGEDYYSVENPANKRRSTLITVLNISE 300  
 IESRFPYKHPPTCFKNTHG[DAAYIQLIYPVTNMFQKHMIG]CVTLTVIIVCSVFIYKIFK 360  
 IDIVLWYRDSYDFLPKASDGGTYDAYILYPTVGEGSTSDCDIFVFKVLPVLEKQCG 420  
 YKLFYIGRDDYVGEDIVEVINENVKSRRLIILVRETSGFSWLGSSEEQIAMYNALVQ 480  
 DGIRVVLLELEKIQDYEMPESIKPIKQKHGAIRWSGDFTPQGPQSAKTRFWKNVRYHMPV 540  
 QRRSPSSKHQLLSPATKKEKLQREAHVPLG 569

FIG. 4

MTLNCVVSIFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHPLKFNYST 60  
 ↑  
 Ig-like 1 domain →  
 AESAGLTLIWYTRQDRDLESPINFRLPENRISKEEDVLWFRPTLLNDTGNYTCMLRNTT 120  
YCSKVAFPLEVVQKDCSCFNSPMKLPVHKLYIETGIGRITCFNVDGYFPSSVKPTITWYG 180  
 ↑  
 Ig-like 2 →  
CYKIQNFNNVIPEGMNLSPILIALISNNGNYTCVVITYPENGRTPHLTRTLTVKVVGSPKNA 240  
VPPVIHSPNDHVVEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKRPDDITIDVTINE 300  
 ↑  
 Ig-like 3 →  
SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAGEVAKAAKVQKVPAPRYTVEL 360  
 Juxtamembranous  
ACGFGATVLLVVILIVVYHVYWLNVLPYRAHFGTDEITLDGKEYDIYVSYARNAEKEEF 420  
 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSPFIQSRRLLVVLSPNYVLQGTQAL 480  
 LELKAGLENMASRCGNINVLVQYXAVKETVKELKRAITVLTVIKWKGEKSKYPQGRFWK 540  
 QLQVAMPVKKSPRRSSDEQGLSYSSLKNV

FIG. 5

MSKSGGGSPSTSLNGLLPLSAALS LWPSTSGEICGPGIDIRNDYQQLKRLNCTVIEGYLH 60  
 Chaîne α →  
 ILLISKARDYRSYRFPKLTVITEYLLLFVRVAGLES LGDLFPNLT VIRGWKLFYNALVIF 120  
 EMTNLKDIGLNLNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGD 180  
 LCPGTMEKPMCKEKTITINNEYNYRCWTTNRCQKMCPCSTCGKRACTENNECCHPECLGSCS 240  
 ↑ Cyst rich domain →  
 APDNDTACVACRHYYAGVCPACPPNTYRFEGWRCVDRDFCANILSAESSDSSEGFVIHD 300  
 GECMQECPSGFIRNGSQSMYCIPCEGSPCPKVC EEEKTKTIDSVTSAQMLQGCTIFKGNL 360  
 ← Cyst rich domain ↑ ↑ L2 domain →  
 LINIRRGNNIASLEENFMGLIEVVTGYVKIRHSHALVSLSF LKRLRLILGEEQLEGNYSP 420  
 YVLDNQNLQQLWDWDHRNLTIKAGKMYFAFPKLCVSEIYRMEEVVTGKGRQSKGDINTR 480  
 NNGERASCESDVLHFTSTTTSKNRIITWHRYRPPDYRD LISFTVYKRAPFKNVTEYDG 540  
 ← L2 ↑ ↑ FbnIII-1 →  
 QDACGSNSWNMVDVLPNKDVEPGILLHGLKFPWTQYAVYVKA VLTMTVENDHIRGAKSE 600  
 ILIYIRTNASVPSIPLDVLASNSSSQLIVKWNPPSLP NGLSYIIVRWQRQPDQGYLYRH 660  
 ← FbnIII-1 ↑ ↑ FbnIII-2a →  
 NYCSKDKIPIRKYADGTIDIEVTENPKTEVC GGEKGPCCAKPCPTRAEKQAEKEEAERYK 720  
 VFENFLHNSIFVPRPERKRDVMQVANITMSSRSRNTTAADTYNITDPERLESTEYFPFES 780  
 ← Juxtamembranaire α  
 ← Chaîne α / Chaîne β →  
 RVDNKERTVISLNRPFPTLYRIDIHSCNHEAKLGCSASN FVFARTMPARGADDIPGPVTW 840  
 ← FbnIII-2b domain → ← FbnIII-2b ↑ ↑ FbnIII-3 →  
 EPRPENSIFLKWPEPENGLILMYEIKYGSQVEDQRECVSRQ EYRKYGKALNRLNPGN 900  
 YTARIQATSLSGNSWTDPVFFVYQAKTGYENFIHLI IALPVAVLLIVGGLVIMLYVFER 960  
 Juxtamembranous β  
 KRNSRLNGVLVYASVNPETPSAADVTVPDWEWEVAREKITMS RELGQSGFMVIEGVAKG 1020  
 VVKDEPETRVAIKTVNEAASMRERIEFLNEASVMKEFNCHHVRL LGVVSQGQPTLVIME 1080

LNTRGDLKSYLRSLRPEMENNPLAPPSLSNMIQMAEIA DGMATLNANKFVHRDLAARN 1140

CMVAEDFTVKIGDFGMTRDIYETDYTRKGGKGLLPVRWMSPESLKDGVTFTTYS DVWSFGV 1200

VLWEIATLAEQPTYQGLSNEQVLRFFVMEGGLLDKPDNCPDMLFELMRMCWQYNPKMRPSFL 1260

EIISSIKEEMEPGFREVSFYYSEENKLPPEBELDLEPENMESVPLDPSASSSSLPLPDRE 1320

SGHKAENGPGPGVLVLRASFDERQPYAHMNGGRKNERALPLPQSTC 1367



β Chain

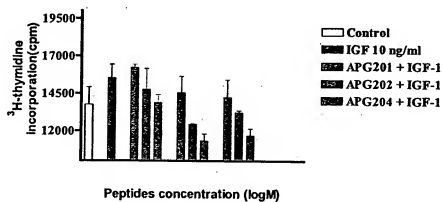
FIG. 6



MGWLCSGLLFPVSCVLVLQVASSGNMKVLQEPTCVSDYMSISTCEWKNNGPTNCSTELRL 60  
 ↑ D1 domain (FbnIII-like) →  
 LYQLVFLLSAHTCIPENNGGAGCVCHLLMDVVSADNYTLDLWAGQQLLWKGSPKPSH 120  
 D1 ← ↑  
 VKPRAPGNLTIVHTNVSDTLTLLTWSNFYPPDNYLYNELTYAVNIWSENDPADFRIYNVTYL 180  
 ↑ D2 domain →  
 EPSLRIAASTLKGISYRARVRWAQCYNTTWSEWSPSTV WHNSYREPFQHLHLLGVSVS 240  
 ← D2 ↑ Juxtamembraneous  
 CIVILAVCLLCYVSITIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEPKACP 300  
 HWKNCCLKLLPCFLEHNMKRDEDPHKAAKEMPPQGSKSAWCFVEISKTVLWPESISVVR 360  
 CVELFEAPVECEEEVEEEKSGFCASPESSRDDPQEGREGIVARLTESFLDLLGEENG 420  
 GFCQQDMGESCLLPFSGSTS AHMPWDEFFSAGPKRAPPWGKEQPLHLESPFPASPTQSPD 480  
 NLTCTETPLVIAGNPAYRSFSNLSQSPCPRGLGPDPLLARHLEEVPEMPQVPLSEPT 540  
 TVPQPEPETWEQILRRNVLQHGAAAAPVSAPTSYQEFVHAVEQGGTQASAVVGLGPPGE 600  
 AGYKAFSSLLASSAVSPKCGFGASSGEGYKFPQDLIPGCGDPAPVVPVPLFTFGLDRE 660  
 PPRSPQSSHLFSSSPEHLGLEPGKEKVEDMPKPLPQEQATDPLVDSLGSIGIVYSALTCHL 720  
 CGHLKQCHQEDGGQTFVMA SPCCGCCGDRSSPPTTFLRAPDPSPGGVPLEASLCFASL 780  
 APSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNVFVSGPTYMRVS 825

FIG. 7

A



B

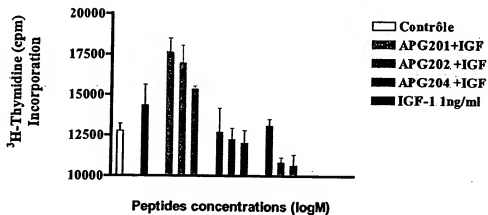
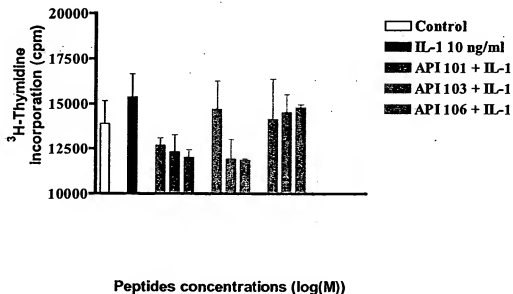


FIG. 8



B

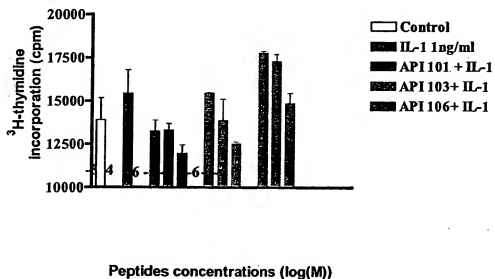


FIG. 9

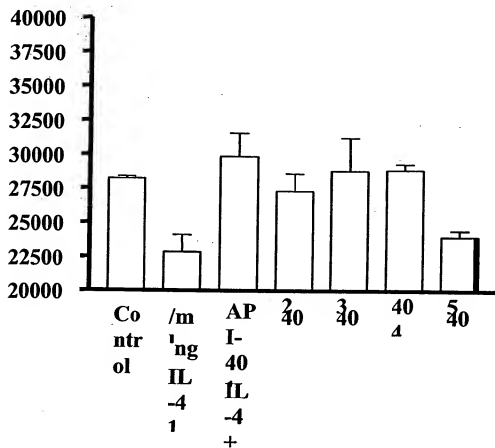


FIG. 10





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VGR2_HUMAN      MQSKVLLAVALMLCVETRAASVGLPSVSLDLPRLSIQDKILTIKANTLLQITCRGQRDL
VGR2_MOUSE      MSSKALLAVALWFCVETRAASVGLPGDFLHPPKLTQDKILTIKANTLLQITCRGQRDL
VGR2_RAT        MSRRALLAVALWFCVETRAASVGLPGDSLHPPKLTQDKILTIKANTLLQITCRGQRDL
VGR2_QUAIL      ---MELGPLRLVLTLLCLAPVAGFLISMDQPTLSIQKSVLTIITNDNLNLTCSQGRAVY
      * . : : * . . . : * * * * : * * * * *

VGR2_HUMAN      WLWPNMQSGSBQRVEVTECS--DGLFCKTLTI PKVIGNDTGAYKCFYRETDLASVIVVVY
VGR2_MOUSE      WLWPNMQRDSBERVLVTECGGSDSIFCKTLTI PRVVGNDTGAYKCSYRVDIASVIVVVY
VGR2_RAT        WLWPNTRPDSBERVLVTECG--DSIFCKTLTVPRVVGNDTGAYKCFYRETDVSSIVIVVVY
VGR2_QUAIL      WSNPNMQSSVEKRLATGCS--EGFPCKTLTLRLVIGNDTGAYKCFYRETDVSSIVIVVVY
      * * * * * : * : * * * . : * * * * : * * * * *

VGR2_HUMAN      QDYSRPFPIASVSDQHGVVYITENKNTVVI PCRGISINLNVSLCARYPEKRFVPGDNRIS
VGR2_MOUSE      RDYSRPFPIASVSDQHGVVYITENKNTVVI PCRGISINLNVSLCARYPEKRFVPGDNRIS
VGR2_RAT        QDHSRPFPIASVSDQHGVVYITENKNTVVI PCRGISINLNVSLCARYPEKRFVPGDNRIS
VGR2_QUAIL      QDYSRPFVTSVGDQLGIVYITKN--KTVVPCIGTVSNLNVSLHAKYPEKRFVPGDGRIS
      : * * * * : * * : * * * * * * * * : * * * * *

VGR2_HUMAN      WDSKKGFTI PSYMI SYAGMVFCEAKINDESYSQSIMYIVVVGYRIYDVVLSPSHGIELSV
VGR2_MOUSE      WDSEIGFTLPSYMI SYAGMVFCEAKINDETSQSIMYIVVVGYRIYDVVLSPPHEIELSA
VGR2_RAT        WDSEKGTFTI PSYMI SYAGMVFCEAKINDETSQSIMYIVLVVGYRIYDVVLSPPHEIELSA
VGR2_QUAIL      WDNKKGFTI PSHLINYAGMVFCEAKIDNESYSQSVIYIVAVVGYRIYDVVLSPPHYQELAV
      * * . : * * * * : * * * * * : * * * * *

VGR2_HUMAN      GEKLVINCTARTELNVGIDFNWEYPSKIQHKLVNRDLKTSQSGSEMKKFLSTLTIDGVT
VGR2_MOUSE      GEKLVINCTARTELNVGLDFTWHSPPSKSHHKI VNRDVKPPFGTVAKMFSLTITIESVT
VGR2_RAT        GEKLVINCTARTELNVGLDFSWQFPSSKHQHKI VNRDVKSLGPTVAKMFSLTITIDSVT
VGR2_QUAIL      GEKLVINACTVKT ELNVGIDFNWDYPSIKERRARTIDRLKTTAG---EIKTFVSLTIESVN
      * * * * * * * * * * * * * : * : : * . . . * * * * *

VGR2_HUMAN      RSDQQLVTCASSGLMTKQNTFVRVHEKPFVAFGSGMESLVEATVGSQVRIPAKYLGVP
VGR2_MOUSE      KSDQCEYTCVASSGRMIKENRTFVRVHTKPFVAFGSGMSLVEATVGSQVRIPVKYLSVP
VGR2_RAT        KSDQCEYTCVAYSLMTKQNTFVRVHTKPFVAFGSGMSLVEATVGSQVRIPVKYLSVP
VGR2_QUAIL      LSDKGRYTCASSGRMMKNSSYFIHESHPFHLEK-MENVVEMKLGDTVSI PVKFKGVP
      * * : * * * * * * : * : : * * * : * : * * * : * *

VGR2_HUMAN      PPEIKWYKNGI PLESNHTIKAGHVLT IMEVSERDTGNVTVILTNPISMEKQSHVSVLVVY
VGR2_MOUSE      APDIKWYRNGRPIESNYTHI VGDELTIMEVTERDAGNYTVILTNPISMEKQSHMVS LVVN
VGR2_RAT        APDIKWYRNGRPIESNYTHI VGDELTIMEVTERDAGNYTVILTNPISMEKQSHMVS LVVN
VGR2_QUAIL      PPEAKWYKNGKVINANHTV KLGVALVITEATEKDAGNYTVILTNPTNKMQRHTFTLLVN
      . * : * * * * : * : * : * * * * * * * * * : * * : * : *

VGR2_HUMAN      VPPQIGEKSLISPVDSYQYGTQTTLCTTYAIPPHIHMYWQLSEECANEPSQAVSVTN
VGR2_MOUSE      VPPQIGEKALISPMDSYQYGTMTLTCTTYANFP LHHIQWYWQLSEACSYRPS----QTS
VGR2_RAT        VPPQIGEKALISPMDSYQYGTMTLTCTTYANFP LHHIQWYWQLSEACSYRPS----QTN
VGR2_QUAIL      VPPQIGENALMAPVDSYKYGSTQALTCTTYAVP PPAVLWYWQLSEECTFS PQKVRIGAN
      * * * * * : * : * * * * * : * * * * * * * : * * * * *

VGR2_HUMAN      PYPCEWRHVSVD PQGNGKI EVNKGQALIEGKHKTVSTLVIQAANVSALYKCEANVKVRG
VGR2_MOUSE      PYACKERHVSVD PQGNGKI EVTKNQYALIEGKHKTVSTLVIQAANVSALYKCEANVKAGR
VGR2_RAT        PYTCKERHVKDPQGNGKI EVTKNQYALIEGKHKTVSTLVIQAANVSALYKCEANVKAGR
VGR2_QUAIL      PYACKRKVKI SERKGNQVEIKQR-VVTIAGKTKTVSTLVIQAANVSALYKCEANVTNRAGS
      * * . * : : : * * * : * . . . * * * * * * * * * * *

VGR2_HUMAN      GERVISFHVTRGPEITLQPMQPTQESVSLMCTADRSTFENLTYKLGQPLPIHVGL
VGR2_MOUSE      GERVISFHVIRGPEITVQPAAPTEQESVSLCTADRNTFENLTYKLGSAQTSVHMGES
VGR2_RAT        GERVISFHVIRGPEITVQPAQPTERESMSLLCTADRNTFENLTYKLGSAQTSVHMGES
VGR2_QUAIL      GERVISFHVTRGLEINLQPRSQLTENKNTSLQCTADKPTFEKLSWYKLSHVSQTPFGGL
      * * * * * * * * * * * * * : * : * * * * : * * * * *

VGR2_HUMAN      PTPVCKNLDLTKLNATMFSN-STNDILIMELKNASLDQDQSYVCLAQDRKTKKRHCVVR
VGR2_MOUSE      LTPVCKNLDALMKGNTMFSN-STNDILIVAFQNASLDQDQSYVCSAQDKTKKRHCLVK
VGR2_RAT        LTPVCKNLDALMKGNTVFSN-STNDILIVAFQNASLDQDQSYVCSAQDKTKKRHCLVK
VGR2_QUAIL      PMPVCKNLDALQKNATVSNVNGENTLELILENISLDQDQSYVCI AQDKTKKRHCLVK
      * * * * * * * * * * * * * : * : * * * * : * * * * *

```

Figure 13





VGR2_HUMAN	DTTVYSSEAEELKLEIGVQTGSTAQILQPDSGTTLSSPPV-----
VGR2_MOUSE	DTTVYSSDEAGLLQMVDAAVHADSGTTLQLTSCINGSGPVPAAPPTPGNHERGAA
VGR2_RAT	DTTVYSSDEAGLLKLVDAVAGHVDSGTTLRSPV-----
VGR2_QUAIL	DNMVCSSDETELLCAQEASPTLPRCAWPGIYSPAPVASLPL-----
	*. * ****: **        2        1

Figure 13 (continued)